Claims

1. A method for identifying a molecular marker useful for detecting tumor cells metastasized from an origin tissue to a destination tissue or fluid, comprising the steps of:

a) down-regulating in a population of origin tissue cells the activity of a transcription factor associated with terminally differentiated origin tissue;

b) comparing an expression profile of the population of down-regulated origin cells with an expression profile of a population of control origin cells;

c) identifying candidate markers which are expressed in the population of control origin cells but not in the population of down-regulated origin cells; and

d) comparing expression of candidate markers in control population of origin cells, cancerous population of origin cells and population of destination cells wherein a candidate marker that is expressed in the population of control origin cells and the population of cancerous origin cells and not in the population of destination cells is useful as a molecular marker for the detection of cancer metastasized from the origin tissue to the destination tissue or fluid.

2. The method of claim 1 wherein the activity of the transcription factor is down-regulated by a method selected from the group consisting of down-regulating the transcription factor gene, down-regulating the activity of the transcription factor and activating a signaling event that inactivates the transcription factor.

3. The method of claim 1 wherein the population of down-regulated origin cells is derived from a cdx2-null intestinal polyp.

4. The method of claim 1 wherein the molecular marker is a polynucleic acid and the expression profiles are compared by a technique selected from the group consisting of differential display, subtractive hybridization, expression array, Serial Analysis of Gene Expression (SAGE), Rapid Analysis of Gene Expression (RAGE),

Massively Parallel Signature Sequencing (MPSS) and Tandem Arrayed Ligation of Expressed Sequence Tags (TALEST).

5. The method of claim 1 wherein the molecular marker is a protein and the expression profiles are compared by a technique selected from the group consisting of 2-D gel electrophoresis and Isotope-Coded Affinity Tags (ICAT).

6. The method of claim 1 wherein the origin tissue and destination tissue are mammalian.

7. The method of claim 6 wherein the origin tissue and destination tissue are human.

8. The method of claim 1 wherein the control origin cells are from an origin tissue which is selected from the group consisting of colorectal, intestine, stomach, liver, mouth, esophagus, throat, thyroid, skin, brain, kidney, pancreas, breast, cervix, ovary, uterus, testicle, prostate, bone, muscle, bladder and lung.

9. The method of claim 1 wherein the population of control origin cells are a cell line selected from the group consisting of T84, Caco2, HT29, SW480, SW620, NCI H508, SW1116, SW1463, Hep G2, and HeLa.

10. The method of claim 1 wherein the cancerous origin cells are cancer cells from tissue selected from the group consisting of colon, stomach, liver, throat, thyroid, skin, brain and lung.

11. The method of claim 1 wherein the population of cancerous origin cells are a cell line selected from the group consisting of T84, Caco2, HT29, SW480, SW620, NCI H508, SW1116, SW1463, Hep G2, and HeLa.

12. The method of claim 1 wherein the destination tissue or body fluid is selected from the group consisting of lymph node, blood, cerebral spinal fluid, and bone marrow.

13. The method of claim 1 wherein the transcriptional factor is selected from the group consisting of Cdx2, STAT5, NKX3.1, FREAC-1, FREAC-2, Pit1, HNF4, LFB1, IPF1, Isl1 and MyoD.

14. The method of claim 1 which comprises the additional step of isolating the molecular marker of step d.

15. The method of claim 1 wherein the transcription factor gene is isolated by the steps of

a) isolating a transcription factor that binds to the regulatory regions of a gene associated with terminal differentiation of the origin tissue; and

b) isolating the gene that expresses the transcription factor.